RAW SEQUENCE LISTING PATENT APPLICATION US/09/084,691

DATE: 06/05/98 TIME: 13:20:34

INPUT SET: S26411.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

	1			SEQUENCE LISTING
	2		·	
	3	(1)	General	Information: ENTERED APPLICANTS: BUKH, J., MILLER, R.H. AND
	4			
	5 6		(i)	
				PURCELL, R.H.
	7		, , , ,	MINIS OF TWO PARTS WAS FORTER AND DEDUCED
	8 9		(ii)	TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
	10			CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
	11			AND THE USE OF REAGENTS DERIVED FROM THESE
	12			SEQUENCES IN DIAGNOSTIC METHODS AND
	13			VACCINES
	14			**************************************
	15		(iii)	NUMBER OF SEQUENCES: 263
	16		(,	, and the second
	17		(iv)	CORRESPONDENCE ADDRESS:
	18		(,	(A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
	19			(B) STREET: 345 PARK AVENUE
	20			(C) CITY: NEW YORK
	21			(D) STATE: NEW YORK
	22			(E) COUNTRY: USA
	23			(F) ZIP: 10154
	24			
	25		(V)	COMPUTER READABLE FORM:
	26			(A) MEDIUM TYPE: FLOPPY DISK
	27			(B) COMPUTER: IBM PC COMPATIBLE
	28			(C) OPERATING SYSTEM: PC-DOS/MS-DOS
	29			(D) SOFTWARE: WORDPERFECT 5.1
	30			
	31		(vi)	CURRENT APPLICATION DATA:
>	O[C32			(A) APPLICATION NUMBER: TO BE ASSIGNED
	`33			(B) FILING DATE: 26-MAY-1998
	34			
	35		(vii)	PRIOR APPLICATION DATA:
	36			(A) APPLICATION NUMBER: 08/290,665
	37			(B) FILING DATE: 15-AUG-1994
	38			
	39		(Vii)	PRIOR APPLICATION DATA:
	40			(A) APPLICATION NUMBER: 08/086,428
	41			(B) FILING DATE: 29-JUNE-1993
	42			ARTICONOLI / A GRANT TARRODY ARTON
	43		(viii)	ATTORNEY/AGENT INFORMATION:
	44			(A) NAME: RICHARD W. BORK
	45 46			(B) REGISTRATION NUMBER: 36,459
	46			(C) REFERENCE/DOCKET NUMBER: 2026-4116US2

RAW SEQUENCE LISTING PATENT APPLICATION US/09/084,691

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47	(it) MELECOMMINICATION INCOMMITTAN	
48 49	(ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (212) 758-4800	
	, ,	
50	(B) TELEFAX: (212) 751-6849 (C) TELEX: 421792	
51 52	(C) TELEX: 421792	
53	(2) INFORMATION FOR SEO ID NO:1:	
54	(2) INFORMATION FOR SEQ ID NO.1.	
55	(i) SEQUENCE CHARACTERISTICS:	
56	(A) LENGTH: 576 base pairs	
57	(B) TYPE: nucleic acid	
58	(C) STRANDEDNESS: single	
59	(D) TOPOLOGY: linear	
60	(=, ===================================	
61	(vi) ORIGINAL SOURCE:	
62	(A) ORGANISM: homosapiens	
63	(C) INDIVIDUAL ISOLATE: DK7	
64		
65	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
66		
67	TAC CAA GTG CGC AAC TCC ACG GGG CTT TAC CAT GTC ACC	39
68	AAT GAT TGC CCT AAC TCG AGT ATC GTG TAC GAG GCG GCC	78
69	GAT GCC ATC CTG CAC ACT CCG GGG TGT GTC CCT TGC GTT	117
70	CGC GAG GGT AAC GTC TCG AGG TGT TGG GTG GCG ATG ACC	156
71	CCC ACG GTG GCC ACC AGG GAT GGC AAA CTC CCC ACA GCG	195
72	CAG CTT CGA CGT CAC ATC GAT CTG CTC GTC GGG AGT GCC	234
73	ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC CTG TGC GGG	273
74	TCT GTC TTT CTT GTC GGT CAA CTG TTT ACC TTC TCT CCC	312
75	AGG CGC CAC TGG ACG ACG CAA GGC TGC AAT TGT TCT ATC	351
76	TAT CCT GGC CAT ATA ACG GGT CAC CGC ATG GCG TGG GAT	390
77	ATG ATG AAC TGG TCC CCT ACC ACG GCG TTG GTA GTA	429
78	GCT CAG CTG CTC CGG ATC CCG CAA GCC ATC TTG GAC ATG	468
79	ATC GCT GGT GCT CAC TGG GGA GTC CTG GCG GGC ATA GCG	507
80	TAT TTT TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA	546
81	GTG CTG CTA TTT GCC GGC GTC GAC GCG	576
82		
83 84	(2) INFORMATION FOR SEQ ID NO:2:	
85	(2) INFORMATION FOR SEQ ID NO:2:	
86	(i) SEQUENCE CHARACTERISTICS:	
87	(A) LENGTH: 576 base pairs	
88	(B) TYPE: nucleic acid	
89	(C) STRANDEDNESS: single	
90	(D) TOPOLOGY: linear	
91	/=/	
92	(vi) ORIGINAL SOURCE:	
93	(A) ORGANISM: homosapiens	
94	(C) INDIVIDUAL ISOLATE: DK9	
95	, ,	
96	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
97	~	
98	TAC CAA GTA CGC AAC TCC TCG GGC CTC TAC CAT GTC ACC	39
99	AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG GCG GCC	78

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		INPUT SET: S26411.raw
100	GAT GCC ATC CTG CAT TCT CCA GGG TGT GTC CCT TGC GTT	117
101	CGC GAG GGT AAC GCC TCG AAA TGT TGG GTG GCG GTG GCC	156
102	CCC ACG GTG GCC ACC AGG GAC GGC AAG CTC CCC GCA ACG	195
103	CAG CTT CGA CGT CAC ATC GAT CTG CTT GTC GGG AGC GCC	234
104	ACC CTC TGC TCG GCC CTC TAT GTG GGG GAC TTG TGC GGG	273
105	TCT GTC TTC CTT GTC GGC CAA CTG TTC ACC TTC TCC CCC	312
106	AGA CGC CAC TGG ACA ACG CAA GAC TGC AAC TGT TCT ATC	351
107	TAC CCC GGC CAT ATT ACG GGT CAT CGC ATG GCG TGG GAT	390
108	ATG ATG ATG AAC TGG TCC CCT ACA GCA GCG CTG GTA ATG	429
109	GCG CAG CTG CTC AGG ATC CCG CAG GCC ATC TTG GAC ATG	468
110	ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG	507
111	TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC GTG GTG	546
112	GTA CTG TTG CTG TTT ACC GGC GTC GAT GCG	576
113		
114		
115	(2) INFORMATION FOR SEQ ID NO:3:	
116		
117	(i) SEQUENCE CHARACTERISTICS:	
118	(A) LENGTH: 576 base pairs	
119	(B) TYPE: nucleic acid	
120	(C) STRANDEDNESS: single	
121	(D) TOPOLOGY: linear	
122		
123	(vi) ORIGINAL SOURCE:	
124	(A) ORGANISM: homosapiens	
125	(C) INDIVIDUAL ISOLATE: DR1	
126	() GEOVERNOE DEGENERATION GEO. TO NO. 0	
127	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
128	010 011 0M0 000 110 M0M 101 000 0MM M10 01M 0M0 100	. 30
129 130	CAC CAA GTG CGC AAC TCT ACA GGG CTT TAC CAT GTC ACC AAT GAT TGC CCT AAT TCG AGT ATT GTG TAC GAG GCG GCC	39
131	GAT GCC ATC CTG CAC GCG CCG GGG TGT GTC CCT TGC GTT	78 117
131	CGC GAG GGT AAC GCC TCG AGG TGT TGG GTG GCC GTT ACC	156
132	CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG	195
134	CAG CTT CGA CGT CAC ATC GAC CTG CTT GTC GGG AGC GCC	234
135	ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC CTG TGC GGG	273
136	TCT GTC TTC CTT GTC GGT CAA CTG TTC ACC TTT TCT CCC	312
137	AGG CGC CAC TGG ACA ACG CAA GAC TGC AAT TGT TCT ATC	351
138	TAT CCC GGC CAT ATA ACG GGA CAC CGT ATG GCA TGG GAT	390
139	ATG ATG AAC TGG TCC CCT ACG ACA GCG CTG GTA ATG	429
140	GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG	468
141	ATC GCT GGA GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG	507
142	TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC GTG GTA	546
143	GTG CTG TTG CTG TTT GCC GGC GTT GAT GCG	576
144		
145		
146	(2) INFORMATION FOR SEQ ID NO:4:	
147		
148	(i) SEQUENCE CHARACTERISTICS:	
149	(A) LENGTH: 576 base pairs	
150	(B) TYPE: nucleic acid	
151	(C) STRANDEDNESS: single	
152	(D) TOPOLOGY: linear	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/084,691

DATE: 06/05/98 TIME: 13:20:36

INPUT SET: S26411.raw

154														
	(vi) ORIGINAL SOURCE:													
155	(A) ORGANISM: homosapiens													
156				((C) :	INDI	JIDUZ	AL IS	SOLA	re:	DR4			
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158		(x:	i) SI	EQUE	VCE !	DESC	RIPT:	ION:	SEQ	ID I	NO:4	:		
159														
160	CAC	CAA	GTG	CGC	AAC	TCT	ACA	GGG	CTT	TAC	CAT	GTC	ACC	39
161	AAT	GAT	TGC	CCT	AAT	TCG	AGT	ATT	GTG	TAC	GAG	GCG	GCC	78
162	GAT	GCC	ATC	CTG	CAC	ACG	CCG	GGG	TGT	GTC	CCT	TGC	GTT	117
163	CGC	GAG	GGT	AAC	ACC	TCG	AGG	TGT	TGG	GTG	GCG	GTG	ACC	156
164	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAA	CTC	CCC	ACA	ACG	195
165	CAG	CTC	CGA	CGT	CAC	ATC	GAC	CTG	CTT	GTC	GGG	AGC	GCC	234
166	ACC	CTC	TGC	TCG	GCC	CTC	TAC	GTG	GGG	GAC	TTG	TGC	GGG	273
167	TCT	GTC	TTC	CTT	GTC	GGT	CAA	CTG	TTC	ACC	TTC	TCT	CCC	312
168	AGG	CAC	CAC	TGG	ACA	ACG	CAA	GAC	TGC	AAT	TGT	TCC	ATC	351
169	TAT	CCC	GGC	CAT	ATA	ACG	GGC	CAC	CGC	ATG	GCG	TGG	GAT	390
170	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACG	ACA	GCG	CTG	GTA	GTA	429
171	GCT	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCC	ATC	TTG	GAC	ATG	468
172	ATC	GCT	GGT	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
173	TAT	TTC	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	CTG	GTA	546
174	GTG	CTG	TTG	CTG	TTT	GCC	GGC	GTT	GAT	GCG				576
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177	(2)	INF	DRMA'	NOIT	FOR	SEQ	ID 1	NO:5:	:					
178														
179		(i)	SE	QUENC	CE CI	HARA	CTER:	ISTIC	CS:					
180				((A) 1	LENG	ΓH:	576	base	e pa:	irs			
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182						STRAI				cia ingl	Э			
183				((C) :		NDEDI	NESS:	: s:	ingl	9			
				((C) :	STRAI	NDEDI	NESS:	: s:	ingl	Э			
183		(v:	i) 01	RIGII	(C) : (D) :	STRAI FOPOI SOUR(NDEDI LOGY CE:	NESS:	: s: inea:	ingle r				
183 184		(v :	L) 01	RIGII	(C) : (D) :	STRAI FOPOI	NDEDI LOGY CE:	NESS:	: s: inea:	ingle r				
183 184 185		(v:	L) OI	RIGII	(C) : (D) : NAL : (A) (STRAI FOPOI SOUR(NDEDI LOGY CE: NISM	NESS: : li	: s: inea:	ingle r apie				
183 184 185 186		(v:	i) OI	RIGII	(C) : (D) : NAL : (A) (STRAI FOPOI SOUR(ORGAI	NDEDI LOGY CE: NISM	NESS: : li	: s: inea:	ingle r apie	ns			
183 184 185 186 187 188		•	·	RIGII	(C) : (D) ! NAL : (A) ((C) :	STRAI FOPOI SOUR(ORGAI	NDEDI LOGY CE: NISM VIDU	NESS: : li : ho	: s: inear omosa SOLA	ingle r apie: rE:	ns S14	•		
183 184 185 186 187 188 189		(x:	i) SI	RIGII	(C) : (D) :	STRAI FOPOI SOURC ORGAI INDIV	NDEDI LOGY CE: NISM VIDUA	NESS: : li : hc	inear	ingler apier TE:	ns S14 NO:5			
183 184 185 186 187 188 189 190		(X:	i) si gtg	RIGII (EQUEI	(C) : (D) : (A) (C) : (C) : (C) : (AAC	STRAI TOPOI SOURG DRGAI INDIV DESCI	NDEDI LOGY CE: NISM /IDU/ RIPT:	NESS: Line NESS: Line NESS: NES: NE	inear comosa SOLAT	ingler apier TE: ID 1	ns S14 NO:5	GTT		39
183 184 185 186 187 188 189 190 191	AAT	(X: CAA GAT	i) Si GTG TGC	RIGII CEQUEI CGC CCT	(C) S (D) S NAL S (A) C (C) S NCE S AAC AAC	STRAI TOPOI SOURGAI INDIV DESCI TCC TCG	NDEDI LOGY CE: NISM /IDU/ RIPT: ACG AGT	NESS: he AL IS ION: GGG ATT	inear moss SOLAT SEQ CTT GTG	ingler apier TE: TAC TAC	ns S14 NO:5	GTT ACA	GCT	78
183 184 185 186 187 188 189 190 191 192 193	AAT GAT	CAA GAT GCT	GTG TGC ATC	RIGII EQUEI CGC CCT CTA	(C) S (D) S NAL S (A) (C) S NCE S AAC AAC CAC	STRAI FOPOI SOURC DRGAI INDIV DESCI TCC TCC GCT	NDEDI LOGY VISM VIDUA RIPT: ACG AGT CCG	NESS: : ho AL IS ION: GGG ATT GGA	inear comosa SOLAT SEQ CTT GTG TGT	ingler apier TE: TAC GTC	ns S14 NO:5 CAT GAG CCT	GTT ACA TGC	GCT GTT	78 117
183 184 185 186 187 188 189 190 191 192 193	AAT GAT CGT	CAA GAT GCT GAG	GTG TGC ATC GGT	RIGIN EQUEN CGC CCT CTA AAC	(C) S (D) S NAL S (A) (C) S NCE S AAC AAC CAC ACC	STRAI FOPOI SOURG ORGAI INDIV DESCI TCC TCC GCT TCG	NDEDI LOGY TE: NISM /IDU/ RIPT: ACG AGT CCG AGG	NESS: li hc AL IS ION: GGG ATT GGA TGT	omosa SOLAT SEQ CTT GTG TGT	ingler apier TE: TAC TAC GTC GTG	CAT GAG CCT GCG	GTT ACA TGC ATG	GCT GTT ACC	78 117 156
183 184 185 186 187 188 189 190 191 192 193 194 195	AAT GAT CGT CCC	CAA GAT GCT GAG ACG	GTG TGC ATC GGT GTG	RIGIN EQUEN CGC CCT CTA AAC GCC	(C) S (D) S NAL S (A) (C) S NCE S AAC AAC AAC AAC ACC ACC ACC	STRAI TOPOI SOURC DRGAI INDIV DESCI TCC TCG GCT TCG AGG	NDEDI LOGY NISM /IDU/ RIPT: ACG AGT CCG AGG GAC	HESS: In the second sec	inear moss SOLAT SEQ CTT GTG TGT TGG AAA	ingler apier TE: TAC GTC GTG CTC	S14 NO:5 CAT GAG CCT GCG CCC	GTT ACA TGC ATG GCA	GCT GTT ACC ACG	78 117 156 195
183 184 185 186 187 188 189 190 191 192 193 194 195	AAT GAT CGT CCC CAG	CAA GAT GCT GAG ACG CTT	GTG TGC ATC GGT GTG CGA	RIGIN CGC CCT CTA AAC GCC CGT	(C) S (D) S (A) C (C) S NCE S AAC AAC AAC ACC ACC ACC ACC ACC	STRAI TOPOI SOURG DRGAI INDIV DESCH TCC TCG GCT TCG AGG ATC	NDEDI LOGY: NISM /IDU/ RIPT: ACG AGT CCG AGG GAC GAT	HESS: hest	inear moss SOLAT SEQ CTT GTG TGT TGG AAA CTT	ingler apier TAC TAC GTC GTC GTC	S14 NO:5 CAT GAG CCT GCG CCC	GTT ACA TGC ATG GCA AGC	GCT GTT ACC ACG GCC	78 117 156 195 234
183 184 185 186 187 188 189 190 191 192 193 194 195 196	AAT GAT CGT CCC CAG ACC	CAA GAT GCT GAG ACG CTT CTC	GTG TGC ATC GGT GTG CGA TGT	CGC CCT CTA AAC GCC CGT	(C) S (D) S (A) C (C) S NCE S AAC AAC AAC ACC ACC ACC ACC ACC ACC AC	STRAI TOPOI SOURG DRGAI INDIV DESCH TCG GCT TCG AGG ATC CTC	NDEDI LOGY: NISM /IDU/ ACG AGT CCG AGG GAC GAT TAC	HESS: hest	inear moss SOLAT SEQ CTT GTG TGT TGG AAA CTT GGG	ingler r apier TAC TAC GTC GTC GTC GTC	CAT GAG CCT GCG CCC GGG TTG	GTT ACA TGC ATG GCA AGC TGC	GCT GTT ACC ACG GCC GGG	78 117 156 195 234 273
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198	AAT GAT CGT CCC CAG ACC TCT	CAA GAT GCT GAG ACG CTT CTC	GTG TGC ATC GGT GTG CGA TGT	CGC CCT CTA AAC GCC CGT TCG CTT	(C) S (D) S (A) C (C) S (C) S AAC AAC AAC ACC ACC ACC ACC GCC GCC GCC	STRAIN TOPOL SOURCE ORGAN INDIVIDUES CHARGE TCG GCT TCG AGG ATC CTC GGT	NDEDI LOGY: NISM /IDU/ ACG AGT CCG AGG GAC GAT TAC CAG	HESS: hest in the second seco	inear moss solar seq crr grg rgr rgg AAA crr ggg rrr	ingler r apier TE: TAC GTC GTC GTC GAC ACC	CAT GAG CCT GCG CCC GGG TTG	GTT ACA TGC ATG GCA AGC TGC	GCT GTT ACC ACG GCC GGC CCC	78 117 156 195 234 273 312
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199	AAT GAT CGT CCC CAG ACC TCT AGG	CAA GAT GCT GAG CTT CTC GTC	GTG TGC ATC GGT GTG CGA TGT TTT CTC	CGC CCT CTA AAC GCC CGT TCG CTT	(C) S (D) S (A) S (A) S (C) S AAC AAC AAC ACC ACC ACC ACC ACC ACC AC	STRAIN TOPOL SOURCE ORGANISTICS TOCK TOCK GOT TOCK AGG ATCK CTCK GGT ACG	NDEDI LOGY LOGY NISM /IDU/ ACG ACG ACG GAC GAC GAT TAC CAG CAG	HESS: hest in the second seco	E SI INEAT SOLAT SEQ CTT GTG TGT TGG AAA CTT GGG TTT	ingler r apier TE: TAC GTC GTC GTC GAC ACC AAT	CAT GAG CCT GCG CCC GGG TTG TTC TGT	GTT ACA TGC ATG GCA AGC TGC TCT	GCT GTT ACC ACG GCC GGC CCC ATC	78 117 156 195 234 273 312 351
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200	AAT GAT CGT CCC CAG ACC TCT AGG TAT	CAA GAT GCT GAG ACG CTT CTC GTC CGC	GTG TGC ATC GGT GTG CGA TGT TTT CTC GGC	CGC CCT CTA AAC GCC CGT TCG CTT TGG	(C) S (D) S (A) S (A) S (C) S AAC AAC AAC ACC ACC ACC ACC ACC ACC AC	STRAIN TOPOL SOURCE ORGAN INDIVIDUES CHARGE AGG ATC CTC GGT ACG ACG ACG	NDEDI LOGY LOGY NISM /IDU/ ACG ACG ACG GAC GAC GAC CAG CAG CAG	NESS: ION: GGG ATT GGA TGT GGC CTG GTG CTG GAC CAT	E SI INEAT SOLAT SEQ CTT GTG TGT TGG AAA CTT GGG TTT TGC CGC	ingler r apier TE: TAC GTC GTC GTC GAC ACC AAT	CAT GAG CCT GCG CCC GGG TTC TTC TGT	GTT ACA TGC ATG GCA AGC TGC TCT TCT	GCT GTT ACC ACG GCC GGG CCC ATC GAT	78 117 156 195 234 273 312 351
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201	AAT GAT CGT CCC CAG ACC TCT AGG TAT	CAA GAT GCT GAG ACG CTT CTC GTC CGC	GTG TGC ATC GGT GTG CGA TGT TTT CTC GGC ATG	CGC CCT CTA AAC GCC CGT TCG CTT TGG CAT	(C) S (D) S (A) S (A) S (C) S AAC AAC AAC ACC ACC ACC ACC ACC ACC AC	STRAIN TOPOL SOURCE ORGANIAN TOC TOC GCT TCG AGG ATC CTC GGT ACG ACG TCC	NDEDI LOGY: NISM VIDUA RIPT: ACG AGT CCG GAC GAC GAT TAC CAG CAG CAA GGT CCT	NESS: I ho AL IS ION: GGG ATT GGA TGT GGC CTG GTG CTG GAC CAT ACG	E SI INEAT SOLAT SEQ CTT GTG TGT TGG AAA CTT GGG TTT TGC CGC	ingle r apie TE: TAC GTC GTC GTC GAC ACC AAT ATG	CAT GAG CCT GCG TTG TTC TGT GCA CTG	GTT ACA TGC ATG GCA AGC TGC TCT TCT TGG GTA	GCT GTT ACC ACG GCC GGG CCC ATC GAT GTA	78 117 156 195 234 273 312 351 390 429
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202	AAT GAT CGT CCC CAG ACC TCT AGG TAT	CAA GAT GCT GAG ACG CTT CTC GTC CGC	GTG TGC ATC GGT GTG CGA TGT TTT CTC GGC ATG	CGC CCT CTA AAC GCC CGT TCG CTT TGG CAT	(C) S (D) S (A) S (A) S (C) S AAC AAC AAC ACC ACC ACC ACC ACC ACC AC	STRAIN TOPOL SOURCE ORGAN INDIVIDUES CHARGE AGG ATC CTC GGT ACG ACG ACG	NDEDI LOGY: NISM VIDUA RIPT: ACG AGT CCG GAC GAC GAT TAC CAG CAG CAA GGT CCT	NESS: I ho AL IS ION: GGG ATT GGA TGT GGC CTG GTG CTG GAC CAT ACG	E SI INEAT SOLAT SEQ CTT GTG TGT TGG AAA CTT GGG TTT TGC CGC	ingle r apie TE: TAC GTC GTC GTC GAC ACC AAT ATG	CAT GAG CCT GCG TTG TTC TGT GCA CTG	GTT ACA TGC ATG GCA AGC TGC TCT TCT TGG GTA	GCT GTT ACC ACG GCC GGG CCC ATC GAT GTA	78 117 156 195 234 273 312 351
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203	AAT GAT CCC CAG ACC TCT AGG TAT ATG GCT	CAA GAT GCT GAG ACG CTT CTC GTC CGC CCC ATG CAG GCT	GTG TGC ATC GGT GTG CGA TGT TTT CTC GGC ATG CTG	CGC CCT CTA AAC GCC CGT TCG CTT TGG CAT AAC	(C) S (D) S (A) S (A) S (C) S AAC AAC AAC ACC ACC ACC ACC ACC ACC AC	STRAIN TOPON SOURCE ORGAN INDIVIDUAL TOCK TOCK TOCK AGG ATC CTC GGT ACG ACG ACG TCC ATC TGG	NDEDI LOGY LOGY NISM /IDU/ RIPT: ACG AGT CCG GAT TAC CAG CAA GGT CCT CCA GGA	NESS: hoseling the second sec	inear moss SEQ CTT GTG TGG AAA CTT GGG TTT TGC CGC ACG GCC CTA	ingle r apie TE: TAC GTC GTC GTC GAC ACC AAT ATG GCA ATC	CAT GAG CCT GCG TTC TGT GCA CTG TTG GCA CTG GGC	GTT ACA TGC ATG GCA AGC TCT TCT TGG GTA GAT ATA	GCT GTT ACC ACG GCC GGG CCC ATC GAT GTA ATG GCG	78 117 156 195 234 273 312 351 390 429 468 507
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202	AAT GAT CCC CAG ACC TCT AGG TAT ATG GCT	CAA GAT GCT GAG ACG CTT CTC GTC CGC CCC ATG CAG GCT	GTG TGC ATC GGT GTG CGA TGT TTT CTC GGC ATG CTG	CGC CCT CTA AAC GCC CGT TCG CTT TGG CAT AAC	(C) S (D) S (A) S (A) S (C) S AAC AAC AAC ACC ACC ACC ACC ACC ACC AC	STRAIN TOPOL SOURCE ORGANINDIVE TCC TCC GCT TCC GGT ACC GGT ACC ACC ACC ATC ACC ATC	NDEDI LOGY LOGY NISM /IDU/ RIPT: ACG AGT CCG GAT TAC CAG CAA GGT CCT CCA GGA	NESS: hoseling the second sec	inear moss SEQ CTT GTG TGG AAA CTT GGG TTT TGC CGC ACG GCC CTA	ingle r apie TE: TAC GTC GTC GTC GAC ACC AAT ATG GCA ATC	CAT GAG CCT GCG TTC TGT GCA CTG TTG GCA CTG GGC	GTT ACA TGC ATG GCA AGC TCT TCT TGG GTA GAT ATA	GCT GTT ACC ACG GCC GGG CCC ATC GAT GTA ATG GCG	78 117 156 195 234 273 312 351 390 429 468
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203	AAT GAT CCC CAG ACC TCT AGG TAT ATG GCT ATC	CAA GAT GCT GAG ACG CTT CTC GCC CCC ATG CAG GCT TTC	GTG TGC ATC GGT GTG CGA TGT TTT CTC GGC ATG CTG GGT TCC	CGC CCT CTA AAC GCC CGT TCG CTT TGG CAT AAC CTC GCT AAC	(C) S (D) S (A) S (A) S (C) S	STRAIN TOPON SOURCE ORGAN INDIVIDUAL TOCK TOCK TOCK AGG ATC CTC GGT ACG ACG ACG TCC ATC TGG	NDEDI LOGY: NISM /IDU/ RIPT: ACG AGT CCG AGC GAT TAC CAG GAT CCA GGT CCA GGT CCA AGC	NESS: hoteleast line in the second s	inear	ingle r apie TE: ID I TAC GTC GTC GTC GAC ACC AAT ATG GCA ATC GCG AAG	CAT GAG CCT GCG TTC TGT GCA CTG TTG GCA CTG GGC	GTT ACA TGC ATG GCA AGC TCT TCT TGG GTA GAT ATA	GCT GTT ACC ACG GCC GGG CCC ATC GAT GTA ATG GCG	78 117 156 195 234 273 312 351 390 429 468 507

RAW SEQUENCE LISTING PATENT APPLICATION US/09/084,691

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206		
207	(2) THEODWARDON FOR CEO ID MO.C.	
208 209	(2) INFORMATION FOR SEQ ID NO:6:	
210	(i) SEQUENCE CHARACTERISTICS:	
211	(A) LENGTH: 576 base pairs	
212	(B) TYPE: nucleic acid	
213	(C) STRANDEDNESS: single	
214	(D) TOPOLOGY: linear	
215	4 7	
216	(vi) ORIGINAL SOURCE:	
217	(A) ORGANISM: homosapiens	
218	(C) INDIVIDUAL ISOLATE: S18	
219		
220	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
221		
222	TAC CAA GTA CGC AAC TCC ACG GGC CTT TAC CAT GTC ACC	39
223	AAT GAC TGC CCT AAC TCG AGC ATT GTG TAC GAG ACG GCC	78
224	GAT ACC ATC CTA CAC TCT CCG GGG TGT GTC CCT TGC GTT	117
225	CGC GAG GGT AAC GCC TCG AGA TGT TGG GTG CCG GTG GCC	156
226	CCC ACA GTT GCC ACC AGG GAC GGC AAA CTC CCC GCA ACG	195
227 228	CAG CTT CGA CGT CAC ATC GAT CTG CTT GTT GGG AGC GCC ACC CTC TGC TCG GCC CTC TAT GTG GGG GAC CTG TGC GGG	234 273
229	TCT GTC TTT CTT GTC AGC CAG CTG TTC ACT ATC TCC CCC	312
230	AGG CGC CAC TGG ACA ACG CAA GAC TGC AAC TGT TCT ATC	351
231	TAC CCC GGC CAT ATA ACG GGT CAC CGT ATG GCA TGG GAT	390
232	ATG ATG AAC TGG TCC CCT ACA ACG GCG TTG GTA ATA	429
233	GCT CAG CTG CTC AGG GTC CCG CAA GCC GTC TTG GAC ATG	468
234	ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG	507
235	TAT TTC TCC ATG GCG GGG AAC TGG GCG AAG GTC CTG CTA	546
236	GTG CTG TTG CTG TTT GCC GGC GTC GAT GCG	576
237		
238		
239	(2) INFORMATION FOR SEQ ID NO:7:	
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241	(1) SEQUENCE CHARACTERISTICS:	
242	(A) LENGTH: 576 base pairs	
243	(B) TYPE: nucleic acid	
244	(C) STRANDEDNESS: single	
245	(D) TOPOLOGY: linear	
246	(vi) ORIGINAL SOURCE:	
247 248	(VI) ORIGINAL SOURCE: (A) ORGANISM: homosapiens	
249	(C) INDIVIDUAL ISOLATE: SW1	
250	(C) INDIVIDUAL ISOLATE. SWI	
251	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
252	("IT) OPEQUIOD PROCESS ITON, OPE ID NO. 1.	
253	TAC CAA GTA CGC AAC TCC TCG GGC CTT TAC CAT GTC ACC	39
254	AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG ACG GCC	78
255	GAT GCC ATT CTA CAC TCT CCA GGG TGT GTC CCT TGC GTT	117
256	CGC GAG GAT GGC GCC CCG AAG TGT TGG GTG GCG GTG GCC	156
257	CCC ACA GTC GCC ACT AGG GAC GGC AAA CTC CCT GCA ACG	195
258	CAG CTT CGA CGT CAC ATC GAT CTG CTT GTC GGA AGC GCC	234

SEQUENCE VERIFICATION REPORT PATENT APPLICATION *US/09/084,691*

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Wrong application Serial Number

(A) APPLICATION NUMBER: TO BE ASSIGNED